GENOMIC AND TRANSCRIPTOMIC ANALYSIS OF *FICUS RELIGIOSA* REVEALS INSIGHTS INTO CARBON FIXATION PATHWAY AND NEURAL DISEASE PATHWAYS

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SYNOPSIS

Indian subcontinent is rich in plant biodiversity and associated with traditional medicinal practices. *Ficus religiosa* (Peepal tree) is a key stone species, huge semi-evergreen and lives for thousands of years. It belongs to the Moraceace family and to the groups of fig trees. The various parts of *F. religiosa* like bark, leaves, fruits and latex are used in traditional medicine to treat different disease conditions. *F. religiosa* is known for the Buddha's meditation and enlightenment and popularly known as Bodhi Tree.

Peepal tree is generally believed to be unique in photosynthesis pathways in plant Kingdom, it believed to produce oxygen during night and day throughout its life cycle. In addition, its stomata are sunken and giant or hydathode, much larger than the normal stomata where it can store more water molecules. However, limited molecular studies have been carried out on *F. religiosa* to understand its molecular and physiological aspects.

In this study, we aimed to establish the molecular data of *F. religiosa*, using next generation sequencing technology. We have carried-out the whole genome sequencing and transcriptomic sequencing and bioinformatics analyses. We sequenced the entire genome of the fig species *F. religiosa* using two next-generation technology platforms that use shotgun sequencing. Based on ab initio, homology, and mRNA evidence utilized for annotation, the assembled genome resulted in a size of 406 Mb and 35,093 protein-coding genes. The repetitive sequences made up around 53% of the entire genome. The gene expression patterns of the carbon fixation pathway were revealed by RNA sequencing from leaf samples collected at day and night period (2 PM and 2 AM, respectively). As a result, it was shown that the genome of Peepal is closely related to the genus Ficus (*F. carica* and *F. macrocarpa*), and relatively close to the genus *M. notabilis* in the same family. This study has provided the annotated genes and pathways related to carbon fixation, neural disease pathways, molecular, metabolic and physiological pathways.